1/18

2

SEQUENCE LISTING

<110> Chugai Seiyaku Kabushiki Kaisha
<110> University College London
<120> HM 1.24-UTILIZING CANCER VACCINES
<130> M915
<160> 23
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<213> Artificial Sequence
<220>
<223> Synthetic DNA comprising leader sequence and HA coding
sequence
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aattcccacc atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt 60.
ccactcatac ccatacgacg tcccagacta cgctggtacc gcggccgcg 109
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<223> Synthetic DNA comprising leader sequence and HA coding
sequence
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tagetgttge taccaagaag aggatgatac agetecatec catggtggg 109
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<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 3

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<223> Primer														
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ctgctgcagt gagatcccag gatccata	28													
<210> 5														
<211> 396														
<212> DNA														
<213> Homosapiens														
<223> Nucleotide sequence of extracellular domain of so	luble													
HM 1.24 antigenic protein														
<400> 5														
aac agc gag gcc tgc cgg gac ggc ctt cgg gca gtg atg gag tgt cgc	48													
Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg														
1 5 10 15														
aat gtc acc cat ctc ctg caa caa gag ctg acc gag gcc cag aag ggc	96													
Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly														
20 25 30														
ttt cag gat gtg gag gcc cag gcc gcc acc tgc aac cac act gtg atg	144													
Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met														
35 40 45														
gcc cta atg gct tcc ctg gat gca gag aag gcc caa gga caa aag aaa	192													
Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys														
50 55 60														
gtg gag gag ctt gag gga gag atc act aca tta aac cat aag ctt cag	240													
Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln														
65 70 75 80														
gac gcg tct gca gag gtg gag cga ctg aga aga gaa aac cag gtc tta	288													

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
85 90 95
age gtg aga ate geg gae aag aag tae tae eee age tee cag gae tee 336
Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
100 105 110
age tee get geg geg eee eag etg etg att gtg etg etg gge etc age 384
Ser Ser Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
115 120 125
gct ctg ctg cag 396
Ala Leu Leu Gln
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<223> Primer
<400> 6
ataggatect caageggage tggagtectg . 30
<210> 7
<211> 345
<212> DNA
<213> Homosapiens
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terminal-lacking soluble HM 1.24 antigenic protein
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Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
1 5 10 15
aat gtc acc cat ctc ctg caa caa gag ctg acc gag gcc cag aag ggc 96
Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
20 25 30
ttt cag gat gtg gag gcc cag gcc gcc acc tgc aac cac act gtg atg 144

Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met	
35 40 45	
gcc cta atg gct tcc ctg gat gca gag aag gcc caa gga caa aag aaa	192
Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys	
50 55 60	
gtg gag gag ctt gag gga gag atc act aca tta aac cat aag ctt cag	240
Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln	
65 70 75 80	
gac gcg tct gca gag gtg gag cga ctg aga aga gaa aac cag gtc tta	288
Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu	
85 90 95	
age gtg aga ate geg gae aag aag tae tae eee age tee eag gae tee	336
Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser	
100 105 110	
agc tcc gct	345
Ser Ser Ala	
115	
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cetcagaete ggcetgaeee gtggaaagaa	30

<210>	10														
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<212>	DNA														
<213> Artificial Sequence															
<220>															
<223> Nucleotide sequence coding for a fusion protein															
comprising HA peptide and soluble HM 1.24 antigenic protein															
<400>	10														
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Tyr Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Ala	Gly	Thr	Asn	Ser	Glu	Ala	Cys	
1			5					10					15		
cgg gad	ggc	ctt	cgg	gca	gtg	atg	gag	tgt	cgc	aat	gtc	acc	cat	ctc	96
Arg Asp	Gly	Leu	Arg	Ala	Val	Met	Glu	Cys	Arg	Asn	Val	Thr	His	Leu	
		20					25					30			
ctg caa	a caa	gag	ctg	acc	gag	gcc	cag	aag	ggc	ttt	cag	gat	gtg	gag	144
Leu Gl	Gln	Glu	Leu	Thr	Glu	Ala	Gln	Lys	Gly	Phe	Gln	Asp	Val	Glu	
	35					40					45				
gcc cag	g gcc	gcc	acc	tgc	aac	cac	act	gtg	atg	gcc	cta	atg	gct	tcc	192
Ala Glr	Ala	Ala	Thr	Cys	Asn	His	Thr	Val	Met	Ala	Leu	Met	Ala	Ser	
50)				55					60					
ctg gat	gca	gag	aag	gcc	caa	gga	caa	aag	aaa	gtg	gag	gag	ctt	gag	240
Leu Asp	Ala	Glu	Lys	Ala	Gln	Gly	Gln	Lys	Lys	Val	Glu	Glu	Leu	Glu	
65				70					75					80	
gga ga	g atc	act	aca	tta	aac	cat	aag	ctt	cag	gac	gcg	tct	gca	gag	288
Gly Glu	ı Ile	Thr	Thr	Leu	Asn	His	Lys	Leu	Gln	Asp	Ala	Ser	Ala	Glu	
			85					90					95		
gtg gag															336
Val Glu	ı Arg	Leu	Arg	Arg	Glu	Asn	Gln	Val	Leu	Ser	Val	Arg	Ile	Ala	
		100					105					110			
gac aag															384
Asp Lys	s Lys	Tyr	Tyr	Pro	Ser	Ser	Gln	Asp	Ser	Ser		Ala	Ala	Ala	
	115					120					125				
ccc cag	gctg	ctg	att	gtg	ctg	ctg	ggc	ctc	agc	gct	ctg	ctg	cag		429

Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln											
130 135 140											
<210> 11											
<211> 378											
<212> DNA											
<213> Artificial Sequence											
<223> Nucleotide sequence coding for a fusion protein											
comprising HA peptide and C-terminal- lacking soluble HM 1.24											
antigenic protein											
<400> 11											
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Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys											
1 5 10 15											
cgg gac ggc ctt cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc 96											
Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu											
20 25 30											
ctg caa caa gag ctg acc gag gcc cag aag ggc ttt cag gat gtg gag 144											
Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu											
35 40 45											
gcc cag gcc gcc acc tgc aac cac act gtg atg gcc cta atg gct tcc 192											
Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser											
50 55 60											
ctg gat gca gag aag gcc caa gga caa aag aaa gtg gag gag ctt gag 240											
Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu											
65 70 7 5 80											
gga gag atc act aca tta aac cat aag ctt cag gac gcg tct gca gag 288											
Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu											
85 90 95											
gtg gag cga ctg aga aga gaa aac cag gtc tta agc gtg aga atc gcg 336											
Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala											
100 105 110											
gac aag aag tac tac eee age tee eag gae tee age tee get											

Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala	
115 120 125	
<210> 12	
<211> 379	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Nucleotide sequence coding for L chain V region vers	ion
a of humamized anti-HM 1.24 antibady	
<400> 12	
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Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-15 -10 -5	
gto cac too gao ato cag atg aco cag ago cca ago ago ctg ago goo	6
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
ago gtg ggt gao aga gtg aco ato aco tgt aag got agt cag gat gtg 14	4
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val	
15 20 25	
aat act get gta gee tgg tae eag eag aag eea gga aag get eea aag 193	2
Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40 45	
ctg ctg atc tac tcg gca tcc aac cgg tac act ggt gtg cca agc aga 24	o
Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg	
50 55 60	_
tte age ggt age ggt ace gae tte ace tte ace ate age age 28	В
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	c
ctc cag cca gag gac atc gct acc tac tac tgc cag caa cat tat agt 33	0
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser	
80 85 90	۵
act cca ttc acg ttc ggc caa ggg acc aag gtg gaa atc aaa c 37	y

Thr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 105 100 95 <210> 13 <211> 418 <212> DNA <213> Artificial Sequence <220> <223> Nucleotide sequence coding for H chain V region version r of humanized anti-HM 1.24 antibady <400> 13 atg gac tgg acc tgg agg gtc ttc ttc ttg ctg gct gta gct cca ggt 48 Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly -5 -10 -15 96 get cae tee cag gtg cag etg gtg cag tet ggg get gag gtg aag aag Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys cct ggg gcc tca gtg aag gtt tcc tgc aag gca tct gga tac acc ttc 144 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe 25 15 20 act ccc tac tgg atg cag tgg gtg cga cag gcc cct gga caa ggg ctt 192 Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu 40 35 30 gag tgg atg gga tct att ttt cct gga gat ggt gat act agg tac agt 240 Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser 60 55 50 cag aag ttc aag ggc aga gtc acc atg acc gca gac aag tcc acg agc 288 Gln Lys Phe Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser 7,0 75 65 aca gec tac atg gag etg age etg aga tet gag gae acg gec gtg 336 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 85 tat tac tgt gcg aga gga tta cga cga ggg ggg tac tac ttt gac tac 384

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Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr
95 100 105
tgg ggg caa ggg acc acg gtc acc gtc tcc tca g 418
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
110 115 120
<210> 14
<211> 418
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<213> Artificial Sequence
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<223> Nucleotide sequence coding for H chain V region version
s of humanized anti-HM 1.24 antibady
<400> 14
atg gac tgg acc tgg agg gtc ttc ttc ttg ctg gct gta gct cca ggt 48
Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly
-15 -10 -5
gct cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 96
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
-1 1 5 10
cct ggg gcc tca gtg aag gtt tcc tgc aag gca tct gga tac acc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15 20 25
act ccc tac tgg atg cag tgg gtg cga cag gcc cct gga caa ggg ctt 192
Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30 35 40 45
gag tgg atg gga tct att ttt cct gga gat ggt gat act agg tac agt 240
Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser
50 55 60
cag aag tte aag gge aga gte ace ate ace gea gae aag tee acg age 288
Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
65 70 75
aca gee tae atg gag etg age etg aga tet gag gae aeg gee gtg 336

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10/18

Thr Ala															
	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
	80					85					90				
tat tac	tgt:	gcg	aga	gga	tta	cga	cga	ggg	ggg	tac	tac	ttt	gac	tac	384
Tyr Ty	Cys	Ala	Arg	Gly	Leu	Arg	Arg	Gly	Gly	Tyr	Tyr	Phe	Asp	Tyr	
9!	5				100					105					
tgg gg	g caa	ggg	acc	acg	gtc	acc	gtc	tcc	tca	g					418
Trp Gl	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser						
110				115					120						
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prote	in e	xpre	sse	d or	ı ce	11 1	memb	oran	e						
<400>	15														
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					Me	t Ala	a Se	r Thi	Se	r Ty:	r Ası	y:	r Cys	3	
					:	L			9	5					
aga gt	g ccc	atg	gaa	gac			aag	cgc			ctt	ctg	ctg	ggg	97
aga gt					ggg	gat			tgt	aag					97
					ggg	gat			tgt	aag					97
Arg Va	l Pro	Met	Glu	Asp 15	GJĀ	gat Asp	Lys	Arg	tgt Cys 20	aag Lys	Leu	Leu	Leu	Gly 25	97 145
Arg Va	l Pro	Met ctg	Glu gtg	Asp 15 ctc	ggg Gly	gat Asp atc	Lys atc	Arg gtg	tgt Cys 20 att	aag Lys ctg	Leu ggg	Leu gtg	Leu	Gly 25 ttg	
Arg Va	l Pro	Met ctg	Glu gtg	Asp 15 ctc	ggg Gly	gat Asp atc	Lys atc	Arg gtg	tgt Cys 20 att	aag Lys ctg	Leu ggg	Leu gtg	Leu	Gly 25 ttg	
Arg Va	l Pro a att	Met ctg Leu	gtg Val	Asp 15 ctc Leu	ggg Gly ctg Leu	gat Asp atc Ile	Lys atc Ile	Arg gtg Val 35	tgt Cys 20 att Ile	aag Lys ctg Leu	Leu ggg Gly	Leu gtg Val	Leu ccc Pro	Gly 25 ttg Leu	
Arg Value 10 ata gg	Pro a att Tle	Met ctg Leu	gtg Val 30	Asp 15 ctc Leu	ggg Gly ctg Leu gcc	gat Asp atc Ile	Lys atc Ile	Arg gtg Val 35 gag	tgt Cys 20 att Ile gcc	aag Lys ctg Leu	ggg Gly	Leu gtg Val gac	ccc Pro 40	Gly 25 ttg Leu ctt	145
Arg Value 10 ata gga Ile Glanda att att	Pro a att Tle	Met ctg Leu	gtg Val 30	Asp 15 ctc Leu	ggg Gly ctg Leu gcc	gat Asp atc Ile	Lys atc Ile	Arg gtg Val 35 gag	tgt Cys 20 att Ile gcc	aag Lys ctg Leu	ggg Gly	Leu gtg Val gac	ccc Pro 40	Gly 25 ttg Leu ctt	145
Arg Value 10 ata gga Ile Glanda att att	a att	Met ctg Leu acc Thr 45	gtg Val 30 atc	Asp 15 ctc Leu aag	ggg Gly ctg Leu gcc Ala	gat Asp atc Ile aac Asn	Lys atc Ile agc Ser 50	gtg Val 35 gag Glu	tgt Cys 20 att Ile gcc Ala	aag Lys ctg Leu tgc Cys	ggg Gly cgg Arg	gtg Val gac Asp	ccc Pro 40 ggc Gly	Gly 25 ttg Leu ctt Leu	145
Arg Value 10 ata gga Ile Gly att att Ile Ile	Pro a att The ttc	Met ctg Leu acc Thr 45	gtg Val 30 atc Ile	Asp 15 ctc Leu aag Lys	ggg Gly ctg Leu gcc Ala	gat Asp atc Ile aac Asn	Lys atc Ile agc ser 50 gtc	gtg Val 35 gag Glu	tgt Cys 20 att Ile gcc Ala	aag Lys ctg Leu tgc Cys	ggg Gly cgg Arg	gtg Val gac Asp 55	ccc Pro 40 ggc Gly	Cly 25 ttg Leu ctt Leu gag	145
Arg Value 10 ata gg Ile Gl; att att Ile Ile Cgg gc	Pro a att The ttc	Met ctg Leu acc Thr 45	gtg Val 30 atc Ile	Asp 15 ctc Leu aag Lys	ggg Gly ctg Leu gcc Ala	gat Asp atc Ile aac Asn	Lys atc Ile agc ser 50 gtc	gtg Val 35 gag Glu	tgt Cys 20 att Ile gcc Ala	aag Lys ctg Leu tgc Cys	ggg Gly cgg Arg	gtg Val gac Asp 55	ccc Pro 40 ggc Gly	Cly 25 ttg Leu ctt Leu gag	145
Arg Value 10 ata gg Ile Gl; att att Ile Ile Cgg gc	a att y Ile ttc Phe a gtg a Val	Met ctg Leu acc Thr 45 atg	gtg Val 30 atc Ile gag Glu	Asp 15 ctc Leu aag Lys tgt	ggg Gly ctg Leu gcc Ala cgc	gat Asp atc Ile aac Asn aat Asn 65	Lys atc Ile agc Ser 50 gtc Val	gtg Val 35 gag Glu acc	tgt Cys 20 att Ile gcc Ala cat	aag Lys ctg Leu tgc Cys ctc Leu	ggg Gly egg Arg ctg Leu 70	gtg Val gac Asp 55 caa Gln	ccc Pro 40 ggc Gly caa Gln	Cly 25 ttg Leu ctt Leu gag Glu	145
Arg Value 10 ata gg. Ile Gl. att atc Ile Ile Cgg gc. Arg Als	a att y Ile ttc Phe a gtg a Val 60 c gag	Met ctg Leu acc Thr 45 atg Met	gtg Val 30 atc Ile gag Glu	Asp 15 ctc Leu aag Lys tgt Cys	ggg Gly ctg Leu gcc Ala cgc Arg	gat Asp atc Ile aac Asn aat Asn 65	atc Ile agc Ser 50 gtc Val	gtg Val 35 gag Glu acc Thr	tgt Cys 20 att Ile gcc Ala cat His	aag Lys ctg Leu tgc Cys ctc Leu	ggg Gly cgg Arg ctg Leu 70	gtg Val gac Asp 55 caa Gln	ccc Pro 40 ggc Gly caa Gln	Cly 25 ttg Leu ctt Leu gag Glu gcc	145 193 241

Second S																			
90 95 100 105 aag gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act 385 Lys Ala Cln Cly Cln Lys Lys Val Clu Clu Clu Clu Clu Clu Clu Clu Clu Cl		acc	tgc	aac	cac	act	gtg	atg	gcc	cta	atg	gct	tcc	ctg	gat	gca	gag	337	
aag gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile thr 110 115 120 aca tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg 433 Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu 125 130 135 aga aga gaa aac cag gtc tta agc gtg aga acc gcg gcg acc aag aag tac 481 Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr 140 145 150 tac ccc agc tcc cag gac tcc agc tcc gcg gcg gcc cc cag ctg ctg Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu 155 160 165 att gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctgc 582 Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln 170 175 180 acatottgga aggtccgtcc tgctcggtt ttcgcttgaa cattcccttg atctcatcag 642 ttctgagcgg gtcatgggg aacacggtta gcgggagag cacggggtag ccggagaagg 702 gcctctggag cagtctgga ggggccatg ggcagtcct ggtgggga cacagtcgg 762 ttgacccag gctgtctccc tccagagcct ccccccggac atgggtggg cacagtcgg 762 ttgacccag gctgtctccc tccagagcct ccccccggac atgggtggg cacagtcgg 762 ttgacccag gattggga tgggggcgg tggggggg tggggggg tggggggc atgggggg cccccccccttttc 822 tcccaccct gagttggga tgggggcgg tggggggc tggggggc atggctcca aaaaaaaaa aaaaaaaaa aaaaaaaaa 942 acttcctttg agggagagc caccttaaaa aaaaaaaaa aaaaaaaaa aaaaaaaa		Thr	Cys	Asn	His	Thr	Val	Met	Ala	Leu	Met	Ala	Ser	Leu	Asp	Ala	Glu		
Lys Ala Gin Gly Gin Lys Lys Val Glu Glu Glu Glu Glu Glu Ile thr 110 115 120 aca tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg Thr Leu Asn His Lys Leu Gin Asp Ala Ser Ala Glu Val Giu Arg Leu 125 130 135 aga aga gaa aac cag gtc tta agc gtg aga acc gcg gaa aag aag tac Arg Arg Glu Asn Gin Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr 140 145 150 tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg Tyr Pro Ser Ser Gin Asp Ser Ser Ser Ala Ala Ala Pro Gin Leu Leu 155 160 165 att gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctgc The Val Leu Leu Gly Leu Ser Ala Leu Leu Gin 170 175 180 acatottgga aggtccgtcc tgctcggtt ttcgctgaa cattcccttg atctcatcag ftctgagcgg gtcatgggg aacacggtta gcgggagag cacggggtag ccgggagagg gcctctggag caggtctgga ggggccatgg ggcatctg ggtgtgggg cacagtcggg ftctgaccagg gctgtctccc tccagagcct ccccccggac aatgagtcc ccctttttc gggttttttt gcggggggg ttgcttttt ctgggtgtt ttggggggc atggtgtgc tggtgtggg ggttttttt gcggggggg ttgcttttt ctgggtgtt ttggggggc atggtgtgcc tgttgttatg ggttcttttt gagggagagca caccttaaaa aaaaaaaaa aaaaaaaaa aaaaaaaa		90					95					100					105		
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tac ccc age tee cag gae tee age tee get geg geg ccc cag etg etg Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu 155 160 165 att gtg ctg etg gge ete age get etg etg gg tgagatecea ggaagetgge 582 Tle Val Leu Leu Gly Leu Ser Ala Leu Leu Gln 170 175 180 acatettgga aggteegtee tgeteggett ttegettgaa cattecettg ateteateag 642 ttetgagegg gteatgggge aacaeggtta gegggagag caeggggtag ceggagaagg 702 geetetggag caggtetgga ggggecatgg ggcagteetg ggtgtgggga caeagteggg 762 ttgacecagg getgteteee teeagageet eceteeggae aatgagteee eeetettgte 822 teecaceetg agattgggea tggggtgegg tgtggggge atgtgetgee tgtgttatg 882 ggttttttt gegggggggg ttgetttt etggggtett tgageteea aaaaataaac 942 actteettt agggaagagea caeettaaaa aaaaaaaaa aaaaaaaaa aaaaaaate 1002 gggeggeege ea 1014 <210> 16 <211> 132 <212> PRT <213> Homosapiens <223> Amino acid sequence of soluble HM 1.24 antigenic protein	,	Arg	Arg	Glu	Asn	Gln	Val	Leu	Ser	Val	Arg	Ile	Ala	Asp	Lys	Lys	Tyr		
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Asn	Val	Thr	His	Leu	Leu	Gln	Gln	Glu	Leu	Thr	Glu	Ala	Gln	Lys	Gly	
			20					25					30			
Phe	Gln	Asp	Val	Glu	Ala	Gln	Ala	Ala	Thr	Cys	Asn	His	Thr	Val	Met	
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Ala	Leu	Met	Ala	Ser	Leu	Asp	Ala	Glu	Lys	Ala	Gln	Gly	Gln	Lys	Lys	
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Ser	Val	Arg	Ile	Ala	Asp	Lys	Lys	Tyr	Tyr	Pro	Ser	Ser	Gln	Asp	Ser	
			100					105					110			
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1				5					10	_,			~1 .	15	01	
· Asn	Val	Thr		Leu	Leu	Gln	Gln		Leu	Thr	Glu	Ala		тĀг	GTĀ	
			20					25		_	_		30	**- 1	No. b	
Phe	Gln	Asp	Val	Glu	Ala	Gln		Ala	Thr	Cys	Asn		Thr	val	met	
		35			_		40	~ 3			C 3	45	CI.	T	T	
Ala		Met	Ala	Ser	Leu		Ala	Glu	Lys	Ala		GTĀ	GIN	тЛЗ	туѕ	
	50					55					60					

Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln 70 75 65 Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu 90 95 85 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser 105 110 100 Ser Ser Ala 115 <210> 18 <211> 143 <212> PRT <213> Artificial Sequence <220> <223> Amino acid sequence of a fusion protein comprising HA peptide and soluble HM 1.24 antigenic protein <400> 18 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys 15 10 5 Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu 25 30 20 Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu 40 Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser 60 55 Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu 75 70 65 Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu 90 85 Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala 100 105 Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala

120

115

Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln 130 135 140 <210> 19 <211> 126 <212> PRT <213> Artificial Sequence <220> <223> Amino acid sequence of a fusion protein comprising HA peptide and C-terminal lacking soluble HM 1.24 antigenic protein <400> 19 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys 5 10 1 Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu 25 Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu 45 40 Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser 60 55 50 Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu 70 75 65 Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu 90 Val Glu Arg Leu Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala 105 110 100 Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala 125 120 115 <210> 20 <211> 126 <212> PRT <213> Artificial Sequence <220>

<223> Amino acid sequence of L chain V region version a of

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humanized anti-HM 1.24 antibady

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                                   -10
                -15
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                             5
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
                         20
                                            25
Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
                                        40
                     35
Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg
                                                        60
                 50
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
                                 70
             65
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser
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Thr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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                                    -10
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
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                         20
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Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu 40 35 Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser 55 50 Gln Lys Phe Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser 75 65 70 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 85 Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr 100 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser 110 115 120 <210> 22 <211> 139 <212> PRT <213> Artificial Sequence <220> <223> Amino acid sequence of H chain V region version s of humanized anti-HM 1.24 antibady <400> 22 Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly -10 -15 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys 5 -1 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe 20 25 15 Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu 40 30 Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser 55 50 Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser

70

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 85 80 Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr 95 100 105 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser 120 110 115 <210> 23 <211> 180 <212> PRT <213> Homosapiens <223> Amino acid sequence of humam HM 1.24 antigenic protein expressed on cell membrane <400> 23 Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu 25 Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala 45 40 35 Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg 55 50 Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly 70 75 Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met 95 90 85 Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys 105 100 Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln 120 115 Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu 135 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser 160

155

150

145

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Ser Ser Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser 165 170 175

Ala Leu Leu Gln